



1102-98.TXT

SEQUENCE LISTING

<110> Kainoh, Mie  
Tanaka, Toshiaki

<120> Chimeric Proteins, their Heterodimer  
Complexes, and Platelet Substitutes

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<140> 09/155,514

<141> 1998-11-17

<150> WO PCT/JP98/00370

<151> 1998-01-29

<150> JP 9-15118

<151> 1997-01-29

<150> JP-9-234544

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ggc	ccc	gaa	gct	gca	ctc	cgg	gag	acg	gtg	atg	ctg	ttg	ctg	tgc	ctg	96
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aac	tgg	ctc	gcc	aac	gct	tca	gtg	atc	aat	ccc	ggg	gcg	att	tac	aga	288
Asn	Trp	Leu	Ala	Asn	Ala	Ser	Val	Ile	Asn	Pro	Gly	Ala	Ile	Tyr	Arg	
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Cys	Arg	Ile	Gly	Lys	Asn	Pro	Gly	Gln	Thr	Cys	Glu	Gln	Leu	Gln	Leu	
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Tyr	Val	Lys	Lys	Phe	Gly	Glu	Asn	Phe	Ala	Ser	Cys	Gln	Ala	Gly	Ile	
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Tyr	Lys	Ala	Phe	Leu	Asp	Lys	Gln	Asn	Gln	Val	Lys	Phe	Gly	Ser	Tyr	
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Leu	Gly	Tyr	Ser	Val	Gly	Ala	Gly	His	Phe	Arg	Ser	Gln	His	Thr	Thr	
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gaa	gta	gtc	gga	gga	gct	cct	caa	cat	gag	cag	att	ggg	aag	gca	tat	864
Glu	Val	Val	Gly	Gly	Ala	Pro	Gln	His	Glu	Gln	Ile	Gly	Lys	Ala	Tyr	
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ata	ttc	agc	att	gat	gaa	aaa	gaa	cta	aat	atc	tta	cat	gaa	atg	aaa	912
Ile	Phe	Ser	Ile	Asp	Glu	Lys	Glu	Leu	Asn	Ile	Leu	His	Glu	Met	Lys	
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## 1102-98.TXT

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ctc Leu	aat Asn	gca Ala	gat Asp	ggc Gly 325	ttc Phe	tca Ser	gat Asp	ctg Leu	ctc Leu 330	gtg Val	gga Gly	gca Ala	ccc Pro	atg Met 335	cag Gln	1008
agc Ser	acc Thr	atc Ile	aga Arg 340	gag Glu	gaa Glu	gga Gly	aga Arg	gtg Val 345	ttt Phe	gtg Val	tac Tyr	atc Ile	aac Asn 350	tct Ser	ggc Gly	1056
tcg Ser	gga Gly	gca Ala 355	gta Val	atg Met	aat Asn	gca Ala	atg Met 360	gaa Glu	aca Thr	aac Asn	ctc Leu	gtt Val 365	gga Gly	agt Ser	gac Asp	1104
aaa Lys	tat Tyr 370	gct Ala	gca Ala	aga Arg	ttt Phe	ggg Gly 375	gaa Glu	tct Ser	ata Ile	gtt Val	aat Asn 380	ctt Leu	ggc Gly	gac Asp	att Ile	1152
gac Asp 385	aat Asn	gat Asp	ggc Gly	ttt Phe	gaa Glu 390	gat Asp	gtt Val	gct Ala	atc Ile	gga Gly 395	gct Ala	cca Pro	caa Gln	gaa Glu	gat Asp 400	1200
gac Asp	ttg Leu	caa Gln	ggt Gly	gct Ala 405	att Ile	tat Tyr	att Ile	tac Tyr	aat Asn 410	ggc Gly	cgt Arg	gca Ala	gat Asp	ggg Gly 415	atc Ile	1248
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cac His	cct Pro	gag Glu	tca Ser	gta Val 485	aat Asn	aga Arg	acg Thr	aaa Lys	ttt Phe 490	gac Asp	tgt Cys	gtt Val	gaa Glu 495	aat Asn	gga Gly	1488
tgg Trp	cct Pro	tct Ser	gtg Val 500	tgc Cys	ata Ile	gat Asp	cta Leu	aca Thr 505	ctt Leu	tgt Cys	ttc Phe	tca Ser	tat Tyr 510	aag Lys	ggc Gly	1536
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gtg Val 530	aac Asn	aga Arg	aag Lys	gca Ala	gag Glu	tct Ser 535	cca Pro	cca Pro	aga Arg	ttc Phe	tat Tyr 540	ttc Phe	tct Ser	tct Ser	aat Asn	1632
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Val Ile Ser Lys Arg Ser Thr Glu Glu Phe Pro Pro Leu 605 Gln Pro Ile 605	
ctt cag cag aag aaa gaa aaa gac ata atg aaa aaa aca ata aac ttt	1872
Leu Gln Gln Lys Lys Glu Lys 615 Asp Ile Met Lys Lys 620 Thr Ile Asn Phe 610	
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Ala Arg Phe Cys Ala His 630 Glu Asn Cys Ser Ala 635 Asp Leu Gln Val Ser 640 625	
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Ala Lys Ile Gly Phe 645 Leu Lys Pro His Glu Asn Lys Thr Tyr Leu Ala 655 650	
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Val Gly Ser Met Lys Thr Leu Met Leu Asn Val Ser Leu Phe Asn Ala 660 665 670	
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Gly Asp Asp Ala Tyr Glu Thr Thr 680 Leu His Val Lys Leu 685 Pro Val Gly 675	
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Leu Tyr Phe Ile Lys Ile Leu 695 Glu Leu Glu Glu Lys 700 Gln Ile Asn Cys 690	
gaa gtc aca gat aac tct ggc gtg gta caa ctt gac tgc agt att ggc	2160
Glu Val Thr Asp Asn Ser Gly Val Val Gln Leu Asp Cys Ser Ile Gly 705 710 715 720	
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Tyr Ile Tyr Val Asp His Leu Ser Arg Ile Asp Ile Ser Phe Leu Leu 725 730 735	
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Asp Val Ser Ser Leu Ser Arg Ala Glu Glu Asp Leu Ser Ile Thr Val 740 745 750	
cat gct acc tgt gaa aat gaa gag gaa atg gac aat cta aag cac agc	2304
His Ala Thr Cys Glu Asn Glu Glu Glu Met Asp Asn Leu Lys His Ser 755 760 765	
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Arg Val Thr Val Ala Ile Pro 775 Leu Lys Tyr Glu Val Lys Leu Thr Val 770 780	
cat ggg ttt gta aac cca act tca ttt gtg tat gga tca aat gat gaa	2400
His Gly Phe Val Asn Pro Thr Ser Phe Val Tyr 795 Gly Ser Asn Asp Glu 800 785 790	
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Asn Glu Pro Glu Thr Cys Met Val Glu Lys Met Asn Leu Thr Phe His	

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## 1102-98.TXT

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 Cys Val Phe Ala Gln Thr Asp Glu Asn Arg Cys Leu Lys Ala Asn Ala  
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 Lys Ser Cys Gly Glu Cys Ile Gln Ala Gly Pro Asn Cys Gly Trp Cys  
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 Thr Asn Ser Thr Phe Leu Gln Glu Gly Met Pro Thr Ser Ala Arg Cys  
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 Asp Asp Leu Glu Ala Leu Lys Lys Gly Cys Pro Pro Asp Asp Ile  
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 Glu Asn Pro Arg Gly Ser Lys Asp Ile Lys Lys Asn Lys Asn Val Thr  
 85 90 95  
 aac cgt agc aaa gga aca gca gag aag ctc aag cca gag gat att cat 336  
 Asn Arg Ser Lys Gly Thr Ala Glu Lys Leu Lys Pro Glu Asp Ile His  
 100 105 110  
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 Gln Ile Gln Pro Gln Gln Leu Val Leu Arg Leu Arg Ser Gly Glu Pro  
 115 120 125  
 cag aca ttt aca tta aaa ttc aag aga gct gaa gac tat ccc att gac 432  
 Gln Thr Phe Thr Leu Lys Phe Lys Arg Ala Glu Asp Tyr Pro Ile Asp  
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Ser	Glu	Gln	Asn	Cys	Thr	Thr	Pro	Phe	Ser	Tyr	Lys	Asn	Val	Leu	Ser					
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Leu	Thr	Asn	Lys	Gly	Glu	Val	Phe	Asn	Glu	Leu	Val	Gly	Lys	Gln	Arg					
					230					235					240					
ata	tct	gga	aat	ttg	gat	tct	cca	gaa	ggt	ggt	ttc	gat	gcc	atc	atg	768				
Ile	Ser	Gly	Asn	Leu	Asp	Ser	Pro	Glu	Gly	Gly	Phe	Asp	Ala	Ile	Met					
				245					250					255						
caa	ggt	gca	ggt	tgt	gga	tca	ctg	att	ggc	tgg	agg	aat	ggt	aca	cgg	816				
Gln	Val	Ala	Val	Cys	Gly	Ser	Leu	Ile	Gly	Trp	Arg	Asn	Val	Thr	Arg					
			260					265					270							
ctg	ctg	gtg	ttt	tcc	aca	gat	gcc	ggg	ttt	cac	ttt	gct	gga	gat	ggg	864				
Leu	Leu	Val	Phe	Ser	Thr	Asp	Ala	Gly	Phe	His	Phe	Ala	Gly	Asp	Gly					
		275					280					285								
aaa	ctt	ggt	ggc	att	ggt	tta	cca	aat	gat	gga	caa	tgt	cac	ctg	gaa	912				
Lys	Leu	Gly	Gly	Ile	Val	Leu	Pro	Asn	Asp	Gly	Gln	Cys	His	Leu	Glu					
	290					295					300									
aat	aat	atg	tac	aca	atg	agc	cat	tat	tat	gat	tat	cct	tct	att	gct	960				
Asn	Asn	Met	Tyr	Thr	Met	Ser	His	Tyr	Tyr	Asp	Tyr	Pro	Ser	Ile	Ala					
					310					315					320					
cac	ctt	gtc	cag	aaa	ctg	agt	gaa	aat	aat	att	cag	aca	att	ttt	gca	1008				
His	Leu	Val	Gln	Lys	Leu	Ser	Glu	Asn	Asn	Ile	Gln	Thr	Ile	Phe	Ala					
				325					330					335						
gtt	act	gaa	gaa	ttt	cag	cct	gtt	tac	aag	gag	ctg	aaa	aac	ttg	atc	1056				
Val	Thr	Glu	Glu	Phe	Gln	Pro	Val	Tyr	Lys	Glu	Leu	Lys	Asn	Leu	Ile					
			340					345					350							
cct	aag	tca	gca	gta	gga	aca	tta	tct	gca	aat	tct	agc	aat	gta	att	1104				
Pro	Lys	Ser	Ala	Val	Gly	Thr	Leu	Ser	Ala	Asn	Ser	Ser	Asn	Val	Ile					
			355				360					365								
cag	ttg	atc	att	gat	gca	tac	aat	tcc	ctt	tcc	tca	gaa	gtc	att	ttg	1152				
Gln	Leu	Ile	Ile	Asp	Ala	Tyr	Asn	Ser	Leu	Ser	Ser	Glu	Val	Ile	Leu					
					375						380									
gaa	aac	ggc	aaa	ttg	tca	gaa	gga	gta	aca	ata	agt	tac	aaa	tct	tac	1200				
Glu	Asn	Gly	Lys	Leu	Ser	Glu	Gly	Val	Thr	Ile	Ser	Tyr	Lys	Ser	Tyr					
					390					395					400					
tgc	aag	aac	ggg	gtg	aat	gga	aca	ggg	gaa	aat	gga	aga	aaa	tgt	tcc	1248				
Cys	Lys	Asn	Gly	Val	Asn	Gly	Thr	Gly	Glu	Asn	Gly	Arg	Lys	Cys	Ser					
				405				410						415						
aat	att	tcc	att	gga	gat	gag	gtt	caa	ttt	gaa	att	agc	ata	act	tca	1296				



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Asn	Ile	Ser	Ile	Gly	Asp	Glu	Val	Gln	Phe	Glu	Ile	Ser	Ile	Thr	Ser		
			420					425					430				
aat	aag	tgt	cca	aaa	aag	gat	tct	gac	agc	ttt	aaa	att	agg	cct	ctg	1344	
Asn	Lys	Cys	Pro	Lys	Lys	Asp	Ser	Asp	Ser	Phe	Lys	Ile	Arg	Pro	Leu		
		435					440					445					
ggc	ttt	acg	gag	gaa	gta	gag	gtt	att	ctt	cag	tac	atc	tgt	gaa	tgt	1392	
Gly	Phe	Thr	Glu	Glu	Val	Glu	Val	Ile	Leu	Gln	Tyr	Ile	Cys	Glu	Cys		
	450					455					460						
gaa	tgc	caa	agc	gaa	ggc	atc	cct	gaa	agt	ccc	aag	tgt	cat	gaa	gga	1440	
Glu	Cys	Gln	Ser	Glu	Gly	Ile	Pro	Glu	Ser	Pro	Lys	Cys	His	Glu	Gly		
465					470					475					480		
aat	ggg	aca	ttt	gag	tgt	ggc	gcg	tgc	agg	tgc	aat	gaa	ggg	cgt	gtt	1488	
Asn	Gly	Thr	Phe	Glu	Cys	Gly	Ala	Cys	Arg	Cys	Asn	Glu	Gly	Arg	Val		
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ggt	aga	cat	tgt	gaa	tgc	agc	aca	gat	gaa	gtt	aac	agt	gaa	gac	atg	1536	
Gly	Arg	His	Cys	Glu	Cys	Ser	Thr	Asp	Glu	Val	Asn	Ser	Glu	Asp	Met		
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Asp	Ala	Tyr	Cys	Arg	Lys	Glu	Asn	Ser	Ser	Glu	Ile	Cys	Ser	Asn	Asn		
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gga	gag	tgc	gtc	tgc	gga	cag	tgt	gtt	tgt	agg	aag	agg	gat	aat	aca	1632	
Gly	Glu	Cys	Val	Cys	Gly	Gln	Cys	Val	Cys	Arg	Lys	Arg	Asp	Asn	Thr		
	530					535					540						
aat	gaa	att	tat	tct	ggc	aaa	ttc	tgc	gag	tgt	gat	aat	ttc	aac	tgt	1680	
Asn	Glu	Ile	Tyr	Ser	Gly	Lys	Phe	Cys	Glu	Cys	Asp	Asn	Phe	Asn	Cys		
					550					555					560		
gat	aga	tcc	aat	ggc	tta	att	tgt	gga	gga	aat	ggt	gtt	tgc	aag	tgt	1728	
Asp	Arg	Ser	Asn	Gly	Leu	Ile	Cys	Gly	Gly	Asn	Gly	Val	Cys	Lys	Cys		
				565					570					575			
cgt	gtg	tgt	gag	tgc	aac	ccc	aac	tac	act	ggc	agt	gca	tgt	gac	tgt	1776	
Arg	Val	Cys	Glu	Cys	Asn	Pro	Asn	Tyr	Thr	Gly	Ser	Ala	Cys	Asp	Cys		
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Ser	Leu	Asp	Thr	Ser	Thr	Cys	Glu	Ala	Ser	Asn	Gly	Gln	Ile	Cys	Asn		
		595					600					605					
ggc	cgg	ggc	atc	tgc	gag	tgt	ggt	gtc	tgt	aag	tgt	aca	gat	ccg	aag	1872	
Gly	Arg	Gly	Ile	Cys	Glu	Cys	Gly	Val	Cys	Lys	Cys	Thr	Asp	Pro	Lys		
	610					615					620						
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Phe	Gln	Gly	Gln	Thr	Cys	Glu	Met	Cys	Gln	Thr	Cys	Leu	Gly	Val	Cys		
					630					635					640		
gct	gag	cat	aaa	gaa	tgt	gtt	cag	tgc	aga	gcc	ttc	aat	aaa	gga	gaa	1968	
Ala	Glu	His	Lys	Glu	Cys	Val	Gln	Cys	Arg	Ala	Phe	Asn	Lys	Gly	Glu		
				645					650					655			
aag	aaa	gac	aca	tgc	aca	cag	gaa	tgt	tcc	tat	ttt	aac	att	acc	aag	2016	
Lys	Lys	Asp	Thr	Cys	Thr	Gln	Glu	Cys	Ser	Tyr	Phe	Asn	Ile	Thr	Lys		
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## 1102-98.TXT

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 Val Glu Ser Arg Asp Lys Leu Pro Gln Pro Val Gln Pro Asp Pro Val  
 675 680 685

tcc cat tgt aag gag aag gat gtt gac gac tgt tgg ttc tat ttt acg 2112  
 Ser His Cys Lys Glu Lys Asp Val Asp Asp Cys Trp Phe Tyr Phe Thr  
 690 695 700

tat tca gtg aat ggg aac aac gag gtc atg gtt cat gtt gtg gag aat 2160  
 Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn  
 705 710 715 720

cca gag tgt ccc act ggt cca gag gat ccc gag ctgctggaag caggctcagc 2213  
 Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu  
 725 730

gctcctgcct ggacgcatcc cggctatgca gccccagtc agggcagcaa ggcaggcccc 2273  
 gtctgcctct tcacccggag cctctgccc cccactcat gctcaggag agggctctct 2333  
 ggctttttcc caggctctgg gcaggcacag gctaggtgcc cctaaccag gccctgcaca 2393  
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 ctcccagatt ccagtaactc ccaatcttct ctctgca gag ccc aaa tct tgt gac 2568  
 Glu Pro Lys Ser Cys Asp  
 735

aaa act cac aca tgc cca ccg tgc cca ggtaagccag cccaggcctc 2615  
 Lys Thr His Thr Cys Pro Pro Cys Pro  
 740 745

gccctccagc tcaaggcggg acaggtgccc tagagtagcc tgcattccagg gacaggcccc 2675  
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 Ala Pro Glu Leu Leu Gly  
 750

gga ccg tca gtc ttc ctc ttc ccc cca aaa ccc aag gac acc ctc atg 2779  
 Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met  
 755 760 765

atc tcc cgg acc cct gag gtc aca tgc gtg gtg gtg gac gtg agc cac 2827  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 770 775 780

gaa gac cct gag gtc aag ttc aac tgg tac gtg gac ggc gtg gag gtg 2875  
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 785 790 795 800

cat aat gcc aag aca aag ccg cgg gag gag cag tac aac agc acg tac 2923  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 805 810 815

cgg gtg gtc agc gtc ctc acc gtc ctg cac cag gac tgg ctg aat ggc 2971  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 820 825 830

aag gag tac aag tgc aag gtc tcc aac aaa gcc ctc cca gcc ccc atc 3019  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 835 840 845

gag aaa acc atc tcc aaa gcc aaa ggtgggaccc gtggggtgcg agggccacat 3073  
 Glu Lys Thr Ile Ser Lys Ala Lys  
 850 855

ggacagaggc cggctcggcc caccctctgc cctgagagtg accgctgtac caacctctgt 3133

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Gly Gln Pro Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser	
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cgg gat gag ctg acc aag aac cag gtc agc ctg acc tgc ctg gtc aaa	3229
Arg Asp Glu Leu Thr Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys	
875 880 885	
ggc ttc tat ccc agc gac atc gcc gtg gag tgg gag agc aat ggg cag	3277
Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln	
890 895 900	
ccg gag aac aac tac aag acc acg cct ccc gtg ctg gat tcc gac ggc	3325
Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly	
905 910 915	
tcc ttc ttc ctc tac agc aag ctc acc gtg gac aag agc agg tgg cag	3373
Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln	
920 925 930	
cag ggg aac gtc ttc tca tgc tcc gtg atg cat gag gct ctg cac aac	3421
Gln Gly Asn Val Phe Ser Cys Ser Val Met His Glu Ala Leu His Asn	
935 940 945 950	
cac tac acg cag aag agc ctc tcc ctg tct ccg ggt aaa tga	3463
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&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic DNA oligonucleotide

&lt;400&gt; 8

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&lt;210&gt; 9

&lt;211&gt; 55

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; synthetic DNA oligonucleotide

&lt;400&gt; 9

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&lt;210&gt; 10

&lt;211&gt; 37

&lt;212&gt; DNA

&lt;213&gt; Artificial Sequence

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&lt;223&gt; synthetic DNA oligonucleotide

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 tta gcg ctc agt caa ggc att tta aat tgt tgt ttg gcc tac aat gtt 96  
 Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val  
 20 25 30  
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 Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe  
 35 40 45  
 ggg tat gca gtg cag cag ttt ata aat cca aaa ggc aac tgg tta ctg 192  
 Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu  
 50 55 60

## 1102-98.TXT

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tat Tyr	aaa Lys	tgt Cys	cct Pro	ggt Val 85	gac Asp	cta Leu	tcc Ser	act Thr	gcc Ala 90	aca Thr	tgt Cys	gaa Glu	aaa Lys	cta Leu 95	aat Asn	288
ttg Leu	caa Gln	act Thr	tca Ser 100	aca Thr	agc Ser	att Ile	cca Pro	aat Asn 105	ggt Val	act Thr	gag Glu	atg Met	aaa Lys 110	acc Thr	aac Asn	336
atg Met	agc Ser	ctc Leu 115	ggc Gly	ttg Leu	atc Ile	ctc Leu	acc Thr 120	agg Arg	aac Asn	atg Met	gga Gly	act Thr 125	gga Gly	ggt Gly	ttt Phe	384
ctc Leu	aca Thr 130	tgt Cys	ggt Gly	cct Pro	ctg Leu	tgg Trp 135	gca Ala	cag Gln	caa Gln	tgt Cys	ggg Gly 140	aat Asn	cag Gln	tat Tyr	tac Tyr	432
aca Thr 145	acg Thr	ggt Gly	gtg Val	tgt Cys	tct Ser 150	gac Asp	atc Ile	agt Ser	cct Pro	gat Asp 155	ttt Phe	cag Gln	ctc Leu	tca Ser	gcc Ala 160	480
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aat Asn	ttt Phe	ttg Leu 195	gaa Glu	aaa Lys	ttt Phe	gta Val	caa Gln 200	ggc Gly	ctt Leu	gat Asp	ata Ile	ggc Gly 205	ccc Pro	aca Thr	aag Lys	624
aca Thr	cag Gln 210	gtg Val	ggg Gly	tta Leu	att Ile	cag Gln 215	tat Tyr	gcc Ala	aat Asn	aat Asn	cca Pro 220	aga Arg	gtt Val	gtg Val	ttt Phe	672
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cag Gln	aca Thr	tcc Ser	caa Gln	tat Tyr 245	ggt Gly	ggg Gly	gac Asp	ctc Leu	aca Thr 250	aac Asn	aca Thr	ttc Phe	gga Gly	gca Ala 255	att Ile	768
caa Gln	tat Tyr	gca Ala 260	aga Arg	aaa Lys	tat Tyr	gcc Ala	tat Tyr	tca Ser 265	gca Ala	gct Ala	tct Ser	ggt Gly	ggg Gly 270	cga Arg	cga Arg	816
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ggt Gly	tca Ser 290	atg Met	ttg Leu	aaa Lys	gct Ala	gtg Val 295	att Ile	gat Asp	caa Gln	tgc Cys	aac Asn 300	cat His	gac Asp	aat Asn	ata Ile	912
ctg Leu	agg Arg	ttt Phe	ggc Gly	ata Ile	gca Ala	ggt Val	ctt Leu	ggg Gly	tac Tyr	tta Leu	aac Asn	aga Arg	aac Asn	gcc Ala	ctt Leu	960

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gct Ala	ttt Phe	ggc Gly	tgg Trp	agt Ser 405	ggg Gly	acc Thr	att Ile	gtc Val	cag Gln 410	aag Lys	aca Thr	tct Ser	cat His	ggc Gly 415	cat His	1248			
ttg Leu	atc Ile	ttt Phe	cct Pro 420	aaa Lys	caa Gln	gcc Ala	ttt Phe	gac Asp 425	caa Gln	att Ile	ctg Leu	cag Gln	gac Asp 430	aga Arg	aat Asn	1296			
cac His	agt Ser	tca Ser 435	tat Tyr	tta Leu	ggg Gly	tac Tyr	tct Ser 440	gtg Val	gct Ala	gca Ala	att Ile	tct Ser 445	act Thr	gga Gly	gaa Glu	1344			
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 Gln Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys  
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 545 550 555 560  
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Leu	Leu	Val	Phe	Ser	Thr	Asp	Ala	Gly	Phe	His	Phe	Ala	Gly	Asp	Gly	270	Gly
260	260	260	260	260	260	260	260	260	260	260	260	260	260	260	260	260	260
Lys	Leu	Gly	Gly	Ile	Val	Leu	Pro	Asn	Asp	Gly	Gln	Cys	His	Leu	Glu	285	Glu
275	275	275	275	275	275	275	275	275	275	275	275	275	275	275	275	275	275
Asn	Asn	Met	Tyr	Thr	Met	Ser	His	Tyr	Tyr	Asp	Tyr	Pro	Ser	Ile	Ala	300	Ala
290	290	290	290	290	290	290	290	290	290	290	290	290	290	290	290	290	290
His	Leu	Val	Gln	Lys	Leu	Ser	Glu	Asn	Asn	Ile	Gln	Thr	Ile	Phe	Ala	315	Ala
305	305	305	305	305	305	305	305	305	305	305	305	305	305	305	305	305	305
Val	Thr	Glu	Glu	Phe	Gln	Pro	Val	Tyr	Lys	Glu	Leu	Lys	Asn	Leu	Ile	330	Ile
310	310	310	310	310	310	310	310	310	310	310	310	310	310	310	310	310	310
Pro	Lys	Ser	Ala	Val	Gly	Thr	Leu	Ser	Ala	Asn	Ser	Ser	Asn	Val	Ile	335	Ile
325	325	325	325	325	325	325	325	325	325	325	325	325	325	325	325	325	325
Gln	Leu	Ile	Ile	Asp	Ala	Tyr	Asn	Ser	Leu	Ser	Ser	Glu	Val	Ile	Leu	340	Leu
335	335	335	335	335	335	335	335	335	335	335	335	335	335	335	335	335	335
Glu	Asn	Gly	Lys	Leu	Ser	Glu	Gly	Val	Thr	Ile	Ser	Tyr	Lys	Ser	Tyr	345	Tyr
340	340	340	340	340	340	340	340	340	340	340	340	340	340	340	340	340	340
Cys	Lys	Asn	Gly	Val	Asn	Gly	Thr	Gly	Glu	Asn	Gly	Arg	Lys	Cys	Ser	350	Ser
355	355	355	355	355	355	355	355	355	355	355	355	355	355	355	355	355	355
Asn	Ile	Ser	Ile	Gly	Asp	Glu	Val	Gln	Phe	Glu	Ile	Ser	Ile	Thr	Ser	355	Ser
360	360	360	360	360	360	360	360	360	360	360	360	360	360	360	360	360	360
Asn	Lys	Cys	Pro	Lys	Lys	Asp	Ser	Asp	Ser	Phe	Lys	Ile	Arg	Pro	Leu	360	Leu
365	365	365	365	365	365	365	365	365	365	365	365	365	365	365	365	365	365
Gly	Phe	Thr	Glu	Glu	Val	Glu	Val	Ile	Leu	Gln	Tyr	Ile	Cys	Glu	Cys	365	Cys
370	370	370	370	370	370	370	370	370	370	370	370	370	370	370	370	370	370
Glu	Cys	Gln	Ser	Glu	Gly	Ile	Pro	Glu	Ser	Pro	Lys	Cys	His	Glu	Gly	370	Gly
375	375	375	375	375	375	375	375	375	375	375	375	375	375	375	375	375	375
Asn	Gly	Thr	Phe	Glu	Cys	Gly	Ala	Cys	Arg	Cys	Asn	Glu	Gly	Arg	Val	375	Val
380	380	380	380	380	380	380	380	380	380	380	380	380	380	380	380	380	380
Gly	Arg	His	Cys	Glu	Cys	Ser	Thr	Asp	Glu	Val	Asn	Ser	Glu	Asp	Met	380	Met
385	385	385	385	385	385	385	385	385	385	385	385	385	385	385	385	385	385
Asp	Ala	Tyr	Cys	Arg	Lys	Glu	Asn	Ser	Ser	Glu	Ile	Cys	Ser	Asn	Asn	385	Asn
390	390	390	390	390	390	390	390	390	390	390	390	390	390	390	390	390	390
Gly	Glu	Cys	Val	Cys	Gly	Gln	Cys	Val	Cys	Arg	Lys	Arg	Asp	Asn	Thr	390	Thr
395	395	395	395	395	395	395	395	395	395	395	395	395	395	395	395	395	395
Asn	Glu	Ile	Tyr	Ser	Gly	Lys	Phe	Cys	Glu	Cys	Asp	Asn	Phe	Asn	Cys	395	Cys
400	400	400	400	400	400	400	400	400	400	400	400	400	400	400	400	400	400
Asp	Arg	Ser	Asn	Gly	Leu	Ile	Cys	Gly	Gly	Asn	Gly	Val	Cys	Lys	Cys	400	Cys
405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405	405
Arg	Val	Cys	Glu	Cys	Asn	Pro	Asn	Tyr	Thr	Gly	Ser	Ala	Cys	Asp	Cys	405	Cys
410	410	410	410	410	410	410	410	410	410	410	410	410	410	410	410	410	410
Ser	Leu	Asp	Thr	Ser	Thr	Cys	Glu	Ala	Ser	Asn	Gly	Gln	Ile	Cys	Asn	410	Asn
415	415	415	415	415	415	415	415	415	415	415	415	415	415	415	415	415	415
Gly	Arg	Gly	Ile	Cys	Glu	Cys	Gly	Val	Cys	Lys	Cys	Thr	Asp	Pro	Lys	415	Lys
420	420	420	420	420	420	420	420	420	420	420	420	420	420	420	420	420	420
Phe	Gln	Gly	Gln	Thr	Cys	Glu	Met	Cys	Gln	Thr	Cys	Leu	Gly	Val	Cys	420	Cys
425	425	425	425	425	425	425	425	425	425	425	425	425	425	425	425	425	425
Ala	Glu	His	Lys	Glu	Cys	Val	Gln	Cys	Arg	Ala	Phe	Asn	Lys	Gly	Glu	425	Glu
430	430	430	430	430	430	430	430	430	430	430	430	430	430	430	430	430	430
Lys	Lys	Asp	Thr	Cys	Thr	Gln	Glu	Cys	Ser	Tyr	Phe	Asn	Ile	Thr	Lys	430	Lys
435	435	435	435	435	435	435	435	435	435	435	435	435	435	435	435	435	435
Val	Glu	Ser	Arg	Asp	Lys	Leu	Pro	Gln	Pro	Val	Gln	Pro	Asp	Pro	Val	435	Val
440	440	440	440	440	440	440	440	440	440	440	440	440	440	440	440	440	440
Ser	His	Cys	Lys	Glu	Lys	Asp	Val	Asp	Asp	Cys	Trp	Phe	Tyr	Phe	Thr	440	Thr
445	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445	445
690	690	690	690	690	690	690	690	690	690	690	690	690	690	690	690	690	690

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Tyr Ser Val Asn Gly Asn Asn Glu Val Met Val His Val Val Glu Asn  
 705 710 715 720  
 Pro Glu Cys Pro Thr Gly Pro Glu Asp Pro Glu Glu Pro Lys Ser Cys  
 725 730 735  
 Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Leu Leu Gly  
 740 745 750  
 Gly Pro Ser Val Phe Leu Phe Pro Lys Pro Lys Asp Thr Leu Met  
 755 760 765  
 Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser His  
 770 775 780  
 Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly Val Glu Val  
 785 790 795 800  
 His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn Ser Thr Tyr  
 805 810 815  
 Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly  
 820 825 830  
 Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro Ala Pro Ile  
 835 840 845  
 Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val  
 850 855 860  
 Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys Asn Gln Val Ser  
 865 870 875 880  
 Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu  
 885 890 895  
 Trp Glu Ser Asn Gly Gln Pro Glu Asn Tyr Lys Thr Thr Pro Pro  
 900 905 910  
 Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys Leu Thr Val  
 915 920 925  
 Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys Ser Val Met  
 930 935 940  
 His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser  
 945 950 955 960  
 Pro Gly Lys

&lt;210&gt; 34

&lt;211&gt; 1367

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; fusion protein

&lt;400&gt; 34

Met Gly Pro Glu Arg Thr Gly Ala Ala Pro Leu Pro Leu Leu Leu Val  
 1 5 10 15  
 Leu Ala Leu Ser Gln Gly Ile Leu Asn Cys Cys Leu Ala Tyr Asn Val  
 20 25 30  
 Gly Leu Pro Glu Ala Lys Ile Phe Ser Gly Pro Ser Ser Glu Gln Phe  
 35 40 45  
 Gly Tyr Ala Val Gln Gln Phe Ile Asn Pro Lys Gly Asn Trp Leu Leu  
 50 55 60  
 Val Gly Ser Pro Trp Ser Gly Phe Pro Glu Asn Arg Met Gly Asp Val  
 65 70 75 80  
 Tyr Lys Cys Pro Val Asp Leu Ser Thr Ala Thr Cys Glu Lys Leu Asn  
 85 90 95  
 Leu Gln Thr Ser Thr Ser Ile Pro Asn Val Thr Glu Met Lys Thr Asn  
 100 105 110  
 Met Ser Leu Gly Leu Ile Leu Thr Arg Asn Met Gly Thr Gly Gly Phe  
 115 120 125  
 Leu Thr Cys Gly Pro Leu Trp Ala Gln Gln Cys Gly Asn Gln Tyr Tyr  
 130 135 140

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Thr	Thr	Gly	Val	Cys	Ser	Asp	Ile	Ser	Pro	Asp	Phe	Gln	Leu	Ser	Ala
145					150					155					160
Ser	Phe	Ser	Pro	Ala	Thr	Gln	Pro	Cys	Pro	Ser	Leu	Ile	Asp	Val	Val
				165					170					175	
Val	Val	Cys	Asp	Glu	Ser	Asn	Ser	Ile	Tyr	Pro	Trp	Asp	Ala	Val	Lys
			180					185					190		
Asn	Phe	Leu	Glu	Lys	Phe	Val	Gln	Gly	Leu	Asp	Ile	Gly	Pro	Thr	Lys
		195					200					205			
Thr	Gln	Val	Gly	Leu	Ile	Gln	Tyr	Ala	Asn	Asn	Pro	Arg	Val	Val	Phe
	210					215					220				
Asn	Leu	Asn	Thr	Tyr	Lys	Thr	Lys	Glu	Glu	Met	Ile	Val	Ala	Thr	Ser
225					230					235					240
Gln	Thr	Ser	Gln	Tyr	Gly	Gly	Asp	Leu	Thr	Asn	Thr	Phe	Gly	Ala	Ile
				245					250					255	
Gln	Tyr	Ala	Arg	Lys	Tyr	Ala	Tyr	Ser	Ala	Ala	Ser	Gly	Gly	Arg	Arg
			260					265					270		
Ser	Ala	Thr	Lys	Val	Met	Val	Val	Val	Thr	Asp	Gly	Glu	Ser	His	Asp
		275					280					285			
Gly	Ser	Met	Leu	Lys	Ala	Val	Ile	Asp	Gln	Cys	Asn	His	Asp	Asn	Ile
	290					295					300				
Leu	Arg	Phe	Gly	Ile	Ala	Val	Leu	Gly	Tyr	Leu	Asn	Arg	Asn	Ala	Leu
305					310					315					320
Asp	Thr	Lys	Asn	Leu	Ile	Lys	Glu	Ile	Lys	Ala	Ile	Ala	Ser	Ile	Pro
				325					330					335	
Thr	Glu	Arg	Tyr	Phe	Phe	Asn	Val	Ser	Asp	Glu	Ala	Ala	Leu	Leu	Glu
			340					345					350		
Lys	Ala	Gly	Thr	Leu	Gly	Glu	Gln	Ile	Phe	Ser	Ile	Glu	Gly	Thr	Val
		355					360					365			
Gln	Gly	Gly	Asp	Asn	Phe	Gln	Met	Glu	Met	Ser	Gln	Val	Gly	Phe	Ser
	370					375					380				
Ala	Asp	Tyr	Ser	Ser	Gln	Asn	Asp	Ile	Leu	Met	Leu	Gly	Ala	Val	Gly
385					390					395					400
Ala	Phe	Gly	Trp	Ser	Gly	Thr	Ile	Val	Gln	Lys	Thr	Ser	His	Gly	His
				405					410					415	
Leu	Ile	Phe	Pro	Lys	Gln	Ala	Phe	Asp	Gln	Ile	Leu	Gln	Asp	Arg	Asn
			420					425					430		
His	Ser	Ser	Tyr	Leu	Gly	Tyr	Ser	Val	Ala	Ala	Ile	Ser	Thr	Gly	Glu
		435					440					445			
Ser	Thr	His	Phe	Val	Ala	Gly	Ala	Pro	Arg	Ala	Asn	Tyr	Thr	Gly	Gln
	450					455					460				
Ile	Val	Leu	Tyr	Ser	Val	Asn	Glu	Asn	Gly	Asn	Ile	Thr	Val	Ile	Gln
465					470					475					480
Ala	His	Arg	Gly	Asp	Gln	Ile	Gly	Ser	Tyr	Phe	Gly	Ser	Val	Leu	Cys
				485					490					495	
Ser	Val	Asp	Val	Asp	Lys	Asp	Thr	Ile	Thr	Asp	Val	Leu	Leu	Val	Gly
			500					505				510			
Ala	Pro	Met	Tyr	Met	Ser	Asp	Leu	Lys	Lys	Glu	Glu	Gly	Arg	Val	Tyr
		515					520					525			
Leu	Phe	Thr	Ile	Lys	Lys	Gly	Ile	Leu	Gly	Gln	His	Gln	Phe	Leu	Glu
	530					535					540				
Gly	Pro	Glu	Gly	Ile	Glu	Asn	Thr	Arg	Phe	Gly	Ser	Ala	Ile	Ala	Ala
545					550					555					560
Leu	Ser	Asp	Ile	Asn	Met	Asp	Gly	Phe	Asn	Asp	Val	Ile	Val	Gly	Ser
				565					570					575	
Pro	Leu	Glu	Asn	Gln	Asn	Ser	Gly	Ala	Val	Tyr	Ile	Tyr	Asn	Gly	His
			580					585					590		
Gln	Gly	Thr	Ile	Arg	Thr	Lys	Tyr	Ser	Gln	Lys	Ile	Leu	Gly	Ser	Asp
		595					600					605			
Gly	Ala	Phe	Arg	Ser	His	Leu	Gln	Tyr	Phe	Gly	Arg	Ser	Leu	Asp	Gly
	610					615					620				
Tyr	Gly	Asp	Leu	Asn	Gly	Asp	Ser	Ile	Thr	Asp	Val	Ser	Ile	Gly	Ala
625					630					635					640
Phe	Gly	Gln	Val	Val	Gln	Leu	Trp	Ser	Gln	Ser	Ile	Ala	Asp	Val	Ala

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Ile	Glu	Ala	Ser	645	Thr	Pro	Glu	Lys	650	Ile	Thr	Leu	Val	Asn	655	Lys	Asn
Ala	Gln	Ile	Ile	660	Leu	Lys	Leu	Cys	665	Phe	Ser	Ala	Lys	Phe	670	Arg	Pro
Lys	Gln	Asn	Asn	675	Gln	Val	Ala	Ile	680	Val	Tyr	Asn	Ile	Thr	Leu	Asp	Ala
Asp	Gly	Phe	Ser	690	Ser	Arg	Val	Thr	695	Ser	Arg	Gly	Leu	Phe	Lys	Glu	Asn
705	Asn	Glu	Arg	710	Cys	Leu	Gln	Lys	715	Met	Val	Val	Asn	Gln	Ala	Gln	Ser
Asn	Glu	Arg	Cys	725	Ile	Ile	Tyr	Ile	730	Gln	Glu	Pro	Ser	Asp	Val	Val	Asn
Cys	Pro	Glu	His	740	Arg	Val	Asp	Ile	745	Ser	Leu	Glu	Asn	Pro	Gly	Thr	Ser
Ser	Leu	Asp	Leu	755	Ala	Tyr	Ser	Glu	760	Thr	Ala	Lys	Val	Phe	Ser	Ile	Pro
Pro	Ala	Leu	Glu	770	Gly	Glu	Asp	Gly	775	Leu	Cys	Ile	Ser	Asp	Leu	Val	Val
Phe	His	Lys	Asp	785	Cys	Gln	Ile	Pro	790	Ala	Ala	Gln	Glu	Gln	Pro	Phe	Ile
Leu	Asp	Val	Arg	805	Leu	Thr	Phe	Ser	810	Val	Thr	Leu	Lys	Asn	Lys	Lys	Lys
Ser	Asn	Gln	Asn	820	Tyr	Asn	Thr	Gly	825	Ile	Val	Val	Asp	Phe	Ser	Glu	Asn
Arg	Glu	Ser	Ala	835	Phe	Ser	Leu	Pro	840	Val	Asp	Gly	Thr	Glu	Val	Thr	Thr
Leu	Phe	Ala	Ser	850	Gln	Lys	Ser	Val	855	Ala	Cys	Asp	Val	Gly	Tyr	Tyr	Tyr
Cys	Gln	Val	Ala	865	Ala	Ser	Gln	Lys	870	Thr	Phe	Thr	Ile	Asn	Phe	Asp	Asp
Pro	Ala	Leu	Lys	885	Glu	Gln	Gln	Val	890	Thr	Phe	Thr	Ile	Asn	Phe	Asp	Asp
Phe	Asn	Leu	Gln	900	Asn	Leu	Gln	Asn	905	Ala	Ser	Leu	Ser	Phe	Gln	Ala	Ala
Leu	Ser	Glu	Ser	915	Gln	Glu	Glu	Asn	920	Lys	Ala	Asp	Asn	Leu	Val	Asn	Leu
Lys	Ile	Pro	Leu	930	Leu	Tyr	Asp	Ala	935	Glu	Ile	His	Leu	Thr	Arg	Ser	Thr
Asn	Ile	Asn	Phe	945	Tyr	Glu	Ile	Ser	950	Ser	Ser	Asp	Gly	Asn	Val	Pro	Ser
Val	His	Ser	Phe	965	Glu	Asp	Val	Gly	970	Pro	Lys	Phe	Ile	Phe	Ser	Leu	Lys
Val	Thr	Thr	Gly	980	Ser	Val	Pro	Val	985	Met	Ala	Thr	Val	Ile	Ile	His	His
Ile	Pro	Gln	Tyr	995	Thr	Lys	Glu	Lys	1000	Asn	Pro	Leu	Met	Tyr	Leu	Thr	Gly
Val	Gln	Thr	Asp	1010	Lys	Ala	Gly	Asp	1015	Ile	Ser	Cys	Asn	Ala	Asp	Ile	Asn
Pro	Leu	Lys	Ile	1025	Gly	Gln	Thr	Ser	1030	Ser	Ser	Val	Ser	Phe	Lys	Ser	Glu
Asn	Phe	Arg	His	1045	Lys	Glu	Leu	Asn	1050	Cys	Arg	Thr	Ala	Ser	Cys	Ser	Ser
Asn	Val	Thr	Cys	1060	Trp	Leu	Lys	Asp	1065	His	Met	Lys	Gly	Glu	Tyr	Phe	Phe
Val	Asn	Val	Thr	1075	Thr	Arg	Ile	Trp	1080	Asn	Gly	Thr	Phe	Ala	Ser	Ser	Thr
Phe	Gln	Thr	Val	1090	Gln	Leu	Thr	Ala	1095	Ala	Ala	Glu	Ile	Asn	Thr	Tyr	Asn
Pro	Glu	Ile	Tyr	1105	Val	Ile	Glu	Asp	1110	Asn	Thr	Val	Thr	Ile	Pro	Leu	Met
Ile	Met	Lys	Pro	1125	Glu	Lys	Ala	Glu	1130	Val	Pro	Thr	Asp	Pro	Glu	Glu	Glu
Pro	Lys	Ser	Cys	1140	Asp	Lys	Thr	His	1145	Thr	Cys	Pro	Pro	Cys	Pro	Ala	Pro

## 1102-98.TXT

Glu Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys  
 1155 1160 1165  
 Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val  
 1170 1175 1180  
 Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp  
 1185 1190 1195 1200  
 Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr  
 1205 1210 1215  
 Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp  
 1220 1225 1230  
 Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu  
 1235 1240 1245  
 Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg  
 1250 1255 1260  
 Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr Lys  
 1265 1270 1275 1280  
 Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp  
 1285 1290 1295  
 Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys  
 1300 1305 1310  
 Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser  
 1315 1320 1325  
 Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser  
 1330 1335 1340  
 Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser  
 1345 1350 1355 1360  
 Leu Ser Leu Ser Pro Gly Lys  
 1365